CLAIMS

1. A method of depleting in a sample of double-stranded oligonucleotides a population of double-stranded oligonucleotides containing mismatched bases thereby enriching in said sample a population of double-stranded oligonucleotides containing correctly matched bases, comprising the steps of:

(a) contacting said sample containing double-stranded oligonucleotides with a mismatch recognition protein under conditions to permit the protein to interact with a double-stranded oligonucleotide containing at least one mismatched base; and

(b) collecting double-stranded oligonucleotides that have not interacted with said mismatch recognition protein, thereby depleting the population of double-stranded oligonucleotides containing mismatched bases.

2. The method of claim 1 wherein prior to the step of collecting, having an additional step comprising separating said double-stranded oligonucleotide containing at least one mismatched base that has interacted with said mismatch recognition protein, from double-stranded oligonucleotides that have not interacted with said mismatch recognition protein.

3. The method of claim 1 wherein the double-stranded oligonucleotides of said sample are chemically synthesized.

4. The method of claim 1 wherein the double-stranded oligonucleotides of said sample are enzymatically synthesized.

5. The method of claim 4 wherein prior to the step of contacting, having additional steps comprising denaturing and reannealing said sample of double-stranded oligonucleotides under conditions to permit conversion of the double-stranded

oligonucleotides first to single-stranded oligonucleotides and then to double-stranded oligonucleotides.

6. The method of claim 1 wherein said mismatch recognition protein is immobilized on a solid support.

7. The method of any one of claims 1, 2, 3, 4, 5 or 6 wherein said double-stranded oligonucleotides are double-stranded DNA.

8. The method of claim 7 wherein the DNA is a gene or a portion of a gene.

9. The method of claim 1 or claim 2 wherein said mismatch recognition protein is MutS.

10. The method of claim 1 or claim 2, wherein immediately following step (a) or simultaneous with step (a), contacting said sample with a nucleotide containing biotin under conditions to permit incorporation of the nucleotide into the oligonucleotides that have interacted with said mismatch recognition protein.

11. The method of claim 10 wherein said mismatch recognition protein is CELI endonuclease.

12. The method of claim 10 wherein said mismatch recognition protein is MuA transposase.

13. The method of claim 10 wherein, following contacting said sample with a nucleotide containing biotin, said sample is contacted with an avidin under conditions to permit the avidin to interact with the biotin.

14. The method of claim 13 wherein said avidin is immobilized on a solid support.

15. The method of claim 13 wherein said avidin is streptavidin.

16. A kit for depleting double-stranded oligonucleotides containing mismatched bases from a population of double-stranded oligonucleotides, comprising a mismatch recognition protein, buffer, control oligonucleotides and instructions.

17. The kit of claim 16, further comprising material for separating mismatch protein bound oligonucleotides from unbound oligonucleotides.

18. The kit of claim 16 or claim 17 wherein said double-stranded oligonucleotides are double-stranded DNA.

19. The kit of claim 18 wherein the DNA is a gene or a portion of a gene.